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# Complete Genome Sequence of a Novel Paramyxovirus, Tailam Virus, Discovered in Sikkim Rats

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**We discovered a novel paramyxovirus, Tailam virus, of subfamily *Paramyxovirinae*, in the kidneys and spleens of Sikkim rats. The coding potential of its genome (3′-N-P/V/C-M-F-SH-TM-G-L-5′) is similar to those of Beilong virus and J virus, with putative proteins having 59.1 to 94.4% and 23.8 to 80.1% amino acid identities to those of Beilong virus and J virus, respectively.**

Paramyxoviruses are nonsegmented negative-sense single-stranded RNA viruses divided into two subfamilies, *Paramyxovirinae* and *Pneumovirinae*. *Paramyxovirinae* is currently subdivided into five genera, namely, *Avulavirus*, *Henipavirus*, *Morbillivirus*, *Respirovirus* and *Rubulavirus*, with a few members remaining unclassified. In 2003, two putative "human cDNAs" were identified from an experiment screening for genes upregulated by angiotensin II, using a human kidney mesangial cell line (5). Sequence analysis revealed that they were homologous to the matrix, fusion, and phosphoprotein genes of paramyxoviruses, suggesting the possibility of a novel paramyxovirus (1, 6). Interestingly, it was also found that these sequences, thought to have originated from a human kidney mesangial cell line, were not amplifiable from such cell lines or human kidney samples, but were amplifiable from a rat kidney mesangial cell line (4). Isolation and complete genome sequencing of the virus confirmed that it was a novel paramyxovirus of the *Paramyxovirinae* subfamily, named Beilong virus (BeiPV), most closely related to J virus (JPV) discovered in kidney autoculture of moribund house mouse (2). BeiPV and JPV probably constitute a novel genus in *Paramyxovirinae*.

During the process of a molecular epidemiology study in rodents for paramyxovirus, we discovered a novel paramyxovirus at the Tai Lam country park in Hong Kong, most closely related to, but significantly different from, BeiPV and JPV, in kidneys and spleens of Sikkim rats (*Rattus andamanensis*). We proposed this virus be named "Tailam virus" (TlmPV), and the complete genome of this virus (strain TL8K) was sequenced.

The complete genome of TlmPV was amplified and sequenced using RNA extracted from the kidney of a Sikkim rat positive for TlmPV as a template with the EZ1 virus minikit (QIAgen, Germany). RNA was converted to cDNA by a combined random priming and oligo(dT) priming strategy. cDNA was amplified by degenerate primers designed by our published strategy (3). The 5′ end of the viral genome was confirmed by rapid amplification of cDNA ends (RACE) using the SMARTer RACE cDNA amplification kit (Clontech).

The genome size of TlmPV is 19,152 bases, with a G+C content of 39.6%. Complementarity between the first and last 13 nucleotides in the genome is imperfect, with differences at nucleotides 4, 5, 12, and 13. The 3′ leader and 5′ trailer sequences are 55 and 28 nucleotides, respectively. The TlmPV genome has a conserved trinucleotide intergenic region sequence. It also conforms to the "rule of six" as in other paramyxovirus genomes, with hexamer phase pattern 2-3-4-3-3-4-4-4, similar to those of BeiPV (2-3-4-3-3-4-4-4), and JPV (2-3-4-3-4-1-4-4). Similar to BeiPV and JPV, the genome of TlmPV contains eight genes (3′-N-P/V/C-M-F-SH-TM-G-L-5′). Pairwise alignment of the predicted gene products among TlmPV and other paramyxoviruses showed the highest amino acid identities with BeiPV and JPV, with the N, P/V/C(P), P/V/C(C), P/V/C(V), P/V/C(W), M, F, SH, TM, G, and L proteins of TlmPV having 85.8% and 51.0%, 75.2% and 44.2%, 75.6% and 38.3%, 75.3% and 43.4%, 72.5% and 40.9%, 94.4% and 80.1%, 88.3% and 68.7%, 85.5% and 23.8%, 59.1% and 33.8%, 59.2% and 33.0%, and 88.2% and 73.4% amino acid identities to BeiPV and JPV, respectively. Similar to BeiPV and JPV, the G gene of TlmPV is particularly large, almost twice of those in other paramyxoviruses.

**Nucleotide sequence accession number.** The complete genome of Tailam virus strain TL8K has been sequenced and submitted to GenBank under accession no. JN689227.

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